

## WEST Search History

DATE: Saturday, August 19, 2006

Hide?	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
-------	-----------------	--------------	------------------

*DB=PGPB,USPT; PLUR=YES; OP=ADJ*

<input type="checkbox"/>	L1	(T1R2 and T1R3).clm.	20
--------------------------	----	----------------------	----

END OF SEARCH HISTORY

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 18:11:56 ; Search time 188 Seconds  
(without alignments)  
2067.219 Million cell updates/sec

Title: US-10-035-045-21  
Perfect score: 4443  
Sequence: 1 MGPRAKTICSLFLLWVLAEE.....ERNTPAYFNSMIQGYTMRRD 839

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	4443	100.0	839	3 US-09-897-427A-4	Sequence 4, Appli
2	4443	100.0	839	4 US-10-035-045-21	Sequence 21, Appl
3	4443	100.0	839	4 US-10-179-373-6	Sequence 6, Appli
4	4443	100.0	839	4 US-10-725-103-6	Sequence 6, Appli
5	4443	100.0	839	4 US-10-725-489-6	Sequence 6, Appli
6	4443	100.0	839	4 US-10-725-080A-6	Sequence 6, Appli
7	4443	100.0	839	4 US-10-725-472A-6	Sequence 6, Appli
8	4443	100.0	839	4 US-10-725-276-21	Sequence 21, Appl
9	4443	100.0	839	4 US-10-770-127-198	Sequence 198, App
10	4443	100.0	839	5 US-10-725-284-21	Sequence 21, Appl
11	4443	100.0	839	5 US-10-725-418-6	Sequence 6, Appli
12	4443	100.0	839	5 US-10-679-102-29	Sequence 29, Appl
13	4443	100.0	839	5 US-10-725-475-6	Sequence 6, Appli
14	4443	100.0	839	6 US-11-050-804-4	Sequence 4, Appli
15	4422	99.5	839	4 US-10-246-785-4	Sequence 4, Appli
16	4392.5	98.9	838	3 US-09-927-315-9	Sequence 9, Appli
17	4392.5	98.9	838	4 US-10-190-417-9	Sequence 9, Appli
18	4392.5	98.9	838	5 US-10-679-102-9	Sequence 9, Appli
19	4392.5	98.9	838	5 US-10-645-441-9	Sequence 9, Appli
20	3463.5	78.0	669	4 US-10-124-598-7	Sequence 7, Appli
21	3463.5	78.0	669	4 US-10-096-144-7	Sequence 7, Appli
22	3463.5	78.0	669	4 US-10-225-567A-683	Sequence 683, App
23	3231	72.7	843	3 US-09-927-315-7	Sequence 7, Appli
24	3231	72.7	843	4 US-10-124-598-1	Sequence 1, Appli
25	3231	72.7	843	4 US-10-096-144-1	Sequence 1, Appli
26	3231	72.7	843	4 US-10-246-785-6	Sequence 6, Appli
27	3231	72.7	843	4 US-10-190-417-7	Sequence 7, Appli
28	3231	72.7	843	4 US-10-179-373-17	Sequence 17, Appl
29	3231	72.7	843	4 US-10-436-715-38	Sequence 38, Appl
30	3231	72.7	843	4 US-10-436-715-70	Sequence 70, Appl
31	3231	72.7	843	4 US-10-725-103-17	Sequence 17, Appl

32	3231	72.7	843	4	US-10-725-489-17	Sequence 17, Appl
33	3231	72.7	843	4	US-10-725-080A-17	Sequence 17, Appl
34	3231	72.7	843	4	US-10-725-472A-17	Sequence 17, Appl
35	3231	72.7	843	5	US-10-725-418-17	Sequence 17, Appl
36	3231	72.7	843	5	US-10-679-102-7	Sequence 7, Appli
37	3231	72.7	843	5	US-10-645-441-7	Sequence 7, Appli
38	3231	72.7	843	5	US-10-725-475-17	Sequence 17, Appl
39	3179	71.6	843	3	US-09-927-315-8	Sequence 8, Appli
40	3179	71.6	843	4	US-10-124-598-2	Sequence 2, Appli
41	3179	71.6	843	4	US-10-096-144-2	Sequence 2, Appli
42	3179	71.6	843	4	US-10-190-417-8	Sequence 8, Appli
43	3179	71.6	843	5	US-10-679-102-8	Sequence 8, Appli
44	3179	71.6	843	5	US-10-645-441-8	Sequence 8, Appli
45	2532.5	57.0	661	4	US-10-246-785-5	Sequence 5, Appli

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 18:12:21 ; Search time 22 Seconds  
(without alignments)  
860.228 Million cell updates/sec

Title: US-10-035-045-21  
Perfect score: 4443  
Sequence: 1 MGPRAKTICSLFLLWLVAE.....ERNTPAYFNSMIQGYTMRRD 839

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 96747 seqs, 22556637 residues

Total number of hits satisfying chosen parameters: 96747

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	309.5	7.0	364	7	US-11-293-697-4612	Sequence 4612, Ap	
2	239.5	5.4	944	6	US-10-449-902-46707	Sequence 46707, A	
3	235.5	5.3	637	6	US-10-449-902-45350	Sequence 45350, A	
4	199	4.5	500	6	US-10-449-902-52670	Sequence 52670, A	
5	163	3.7	845	6	US-10-449-902-52662	Sequence 52662, A	
6	104	2.3	1791	7	US-11-313-450-18	Sequence 18, Appl	
7	101.5	2.3	517	6	US-10-449-902-50110	Sequence 50110, A	
8	101.5	2.3	595	6	US-10-449-902-42611	Sequence 42611, A	
9	97	2.2	416	6	US-10-953-349-5363	Sequence 5363, Ap	
10	97	2.2	467	6	US-10-953-349-5362	Sequence 5362, Ap	
11	97	2.2	592	6	US-10-953-349-5361	Sequence 5361, Ap	
12	95	2.1	764	6	US-10-449-902-42792	Sequence 42792, A	
13	94.5	2.1	932	6	US-10-449-902-35289	Sequence 35289, A	
14	94.5	2.1	932	6	US-10-449-902-55200	Sequence 55200, A	
15	94	2.1	950	6	US-10-449-902-52175	Sequence 52175, A	
16	92.5	2.1	500	6	US-10-449-902-28844	Sequence 28844, A	
17	92.5	2.1	580	6	US-10-449-902-43846	Sequence 43846, A	
18	92	2.1	832	6	US-10-449-902-53946	Sequence 53946, A	
19	91	2.0	447	6	US-10-471-571A-5314	Sequence 5314, Ap	
20	90	2.0	691	6	US-10-511-937-2995	Sequence 2995, Ap	
21	89.5	2.0	382	6	US-10-449-902-50854	Sequence 50854, A	
22	89.5	2.0	403	6	US-10-505-928-203	Sequence 203, App	
23	89.5	2.0	435	6	US-10-471-571A-2012	Sequence 2012, Ap	
24	88.5	2.0	827	6	US-10-449-902-47927	Sequence 47927, A	
25	88.5	2.0	858	7	US-11-293-697-2979	Sequence 2979, Ap	
26	88.5	2.0	1033	6	US-10-449-902-55424	Sequence 55424, A	
27	88	2.0	466	6	US-10-471-571A-5276	Sequence 5276, Ap	
28	88	2.0	691	7	US-11-337-061-4	Sequence 4, Appli	
29	87.5	2.0	412	6	US-10-449-902-31469	Sequence 31469, A	

30	87.5	2.0	565	6	US-10-449-902-44962	Sequence 44962, A
31	87.5	2.0	630	7	US-11-313-450-34	Sequence 34, Appl
32	87	2.0	207	6	US-10-449-902-48804	Sequence 48804, A
33	87	2.0	430	6	US-10-953-349-20015	Sequence 20015, A
34	87	2.0	462	6	US-10-953-349-20014	Sequence 20014, A
35	87	2.0	477	6	US-10-953-349-20013	Sequence 20013, A
36	87	2.0	585	6	US-10-449-902-52644	Sequence 52644, A
37	87	2.0	2937	6	US-10-480-962-18	Sequence 18, Appl
38	87	2.0	2969	6	US-10-480-962-19	Sequence 19, Appl
39	86.5	1.9	369	7	US-11-293-697-3609	Sequence 3609, Ap
40	86.5	1.9	504	6	US-10-505-928-42	Sequence 42, Appl
41	86.5	1.9	788	6	US-10-449-902-48805	Sequence 48805, A
42	86.5	1.9	981	6	US-10-471-571A-666	Sequence 666, App
43	86	1.9	385	6	US-10-449-902-49336	Sequence 49336, A
44	86	1.9	454	6	US-10-449-902-49028	Sequence 49028, A
45	86	1.9	542	7	US-11-261-673-2	Sequence 2, Appli

# SCORE Search Results Details for Application 10035045 and Search Result us-10-035-045-21.rapm.

[Score Home](#)    [Retrieve Application](#)    [SCORE System](#)    [SCORE](#)    [Comments /](#)  
[Page](#)    [List](#)    [Overview](#)    [FAQ](#)    [Suggestions](#)

This page gives you Search Results detail for the Application 10035045 and Search Result us-10-035-045-21.rapm.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 18:00:30 ; Search time 612 Seconds  
(without alignments)  
2093.327 Million cell updates/sec

Title: US-10-035-045-21  
Perfect score: 4443  
Sequence: 1 MGPRAKTICSLFLLWVLAE.....ERNTPAYFNSMIQGYTMRD 839

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/paa/PCTUS\_COMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US066\_COMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US073\_COMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US074\_COMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US075\_COMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US076\_COMB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US077\_COMB.pep:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US078\_COMB.pep:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US079\_COMB.pep:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US080\_COMB.pep:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US081\_COMB.pep:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US082\_COMB.pep:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US083\_COMB.pep:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US084\_COMB.pep:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US085\_COMB.pep:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US086\_COMB.pep:\*
- 17: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US087\_COMB.pep:\*
- 18: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US088\_COMB.pep:\*
- 19: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US089\_COMB.pep:\*
- 20: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US090\_COMB.pep:\*
- 21: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US091\_COMB.pep:\*
- 22: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US092\_COMB.pep:\*
- 23: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US093\_COMB.pep:\*
- 24: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US094\_COMB.pep:\*
- 25: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US095\_COMB.pep:\*
- 26: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US096\_COMB.pep:\*
- 27: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US097\_COMB.pep:\*

```

28: /EMC_Celerra_SIDS3/ptodata/2/paa/US098_COMB.pep:*
29: /EMC_Celerra_SIDS3/ptodata/2/paa/US099_COMB.pep:*
30: /EMC_Celerra_SIDS3/ptodata/2/paa/US100_COMB.pep:*
31: /EMC_Celerra_SIDS3/ptodata/2/paa/US101_COMB.pep:*
32: /EMC_Celerra_SIDS3/ptodata/2/paa/US102_COMB.pep:*
33: /EMC_Celerra_SIDS3/ptodata/2/paa/US103_COMB.pep:*
34: /EMC_Celerra_SIDS3/ptodata/2/paa/US104_COMB.pep:*
35: /EMC_Celerra_SIDS3/ptodata/2/paa/US105_COMB.pep:*
36: /EMC_Celerra_SIDS3/ptodata/2/paa/US106_COMB.pep:*
37: /EMC_Celerra_SIDS3/ptodata/2/paa/US107_COMB.pep:*
38: /EMC_Celerra_SIDS3/ptodata/2/paa/US108_COMB.pep:*
39: /EMC_Celerra_SIDS3/ptodata/2/paa/US109_COMB.pep:*
40: /EMC_Celerra_SIDS3/ptodata/2/paa/US110_COMB.pep:*
41: /EMC_Celerra_SIDS3/ptodata/2/paa/US111_COMB.pep:*
42: /EMC_Celerra_SIDS3/ptodata/2/paa/US112_COMB.pep:*
43: /EMC_Celerra_SIDS3/ptodata/2/paa/US113_COMB.pep:*
44: /EMC_Celerra_SIDS3/ptodata/2/paa/US114_COMB.pep:*
45: /EMC_Celerra_SIDS3/ptodata/2/paa/US600_COMB.pep:*
46: /EMC_Celerra_SIDS3/ptodata/2/paa/US601_COMB.pep:*
47: /EMC_Celerra_SIDS3/ptodata/2/paa/US602_COMB.pep:*
48: /EMC_Celerra_SIDS3/ptodata/2/paa/US603_COMB.pep:*
49: /EMC_Celerra_SIDS3/ptodata/2/paa/US604_COMB.pep:*
50: /EMC_Celerra_SIDS3/ptodata/2/paa/US605_COMB.pep:*
51: /EMC_Celerra_SIDS3/ptodata/2/paa/US606_COMB.pep:*
52: /EMC_Celerra_SIDS3/ptodata/2/paa/US607_COMB.pep:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	4443	100.0	839	1	PCT-US04-02987-198	Sequence 198, App
2	4443	100.0	839	1	PCT-US04-25459-6	Sequence 6, Appli
3	4443	100.0	839	1	PCT-US04-32678-29	Sequence 29, Appl
4	4443	100.0	839	30	US-10-035-045-21	Sequence 21, Appl
5	4443	100.0	839	31	US-10-179-373-6	Sequence 6, Appli
6	4443	100.0	839	36	US-10-679-102-29	Sequence 29, Appl
7	4443	100.0	839	37	US-10-725-037-6	Sequence 6, Appli
8	4443	100.0	839	37	US-10-725-080A-6	Sequence 6, Appli
9	4443	100.0	839	37	US-10-725-103-6	Sequence 6, Appli
10	4443	100.0	839	37	US-10-725-276-21	Sequence 21, Appl
11	4443	100.0	839	37	US-10-725-284-21	Sequence 21, Appl
12	4443	100.0	839	37	US-10-725-418-6	Sequence 6, Appli
13	4443	100.0	839	37	US-10-725-472A-6	Sequence 6, Appli
14	4443	100.0	839	37	US-10-725-475-6	Sequence 6, Appli
15	4443	100.0	839	37	US-10-725-488-6	Sequence 6, Appli
16	4443	100.0	839	37	US-10-725-489-6	Sequence 6, Appli
17	4443	100.0	839	40	US-11-050-804-4	Sequence 4, Appli
18	4443	100.0	839	49	US-60-482-992-20	Sequence 20, Appl
19	4443	100.0	839	50	US-60-554-751-20	Sequence 20, Appl
20	4443	100.0	839	52	US-60-710-726-2	Sequence 2, Appli
21	4443	100.0	839	52	US-60-751-420-42	Sequence 42, Appl
22	4423	99.5	839	52	US-60-793-521-10	Sequence 10, Appl
23	4423	99.5	839	52	US-60-793-686-2	Sequence 2, Appli
24	4422	99.5	839	32	US-10-246-785-4	Sequence 4, Appli
25	4392.5	98.9	838	1	PCT-US02-21269-9	Sequence 9, Appli
26	4392.5	98.9	838	1	PCT-US04-32678-9	Sequence 9, Appli
27	4392.5	98.9	838	29	US-09-927-315-9	Sequence 9, Appli
28	4392.5	98.9	838	31	US-10-190-417-9	Sequence 9, Appli
29	4392.5	98.9	838	36	US-10-645-441-9	Sequence 9, Appli
30	4392.5	98.9	838	36	US-10-679-102-9	Sequence 9, Appli
31	4146.5	93.3	838	1	PCT-US04-25459-16	Sequence 16, Appl
32	4146.5	93.3	838	1	PCT-US04-25459-22	Sequence 22, Appl
33	3597	81.0	678	31	US-10-170-205E-26489	Sequence 26489, A
34	3597	81.0	678	47	US-60-245-225-365	Sequence 365, App
35	3597	81.0	678	49	US-60-452-680-21000	Sequence 21000, A
36	3597	81.0	678	49	US-60-453-050-12736	Sequence 12736, A
37	3597	81.0	678	49	US-60-453-135-12736	Sequence 12736, A
38	3597	81.0	678	49	US-60-466-412-12736	Sequence 12736, A
39	3564	80.2	682	47	US-60-248-505-716	Sequence 716, App
40	3506	78.9	843	1	PCT-US04-25459-23	Sequence 23, Appl
41	3495.5	78.7	844	1	PCT-US04-25459-17	Sequence 17, Appl

42	3463.5	78.0	669	30	US-10-096-144-7	Sequence 7, Appli
43	3463.5	78.0	669	31	US-10-124-598-7	Sequence 7, Appli
44	3463.5	78.0	669	32	US-10-225-567A-683	Sequence 683, App
45	3398.5	76.5	840	1	PCT-US04-25459-26	Sequence 26, Appl

## ALIGNMENTS

## RESULT 1

PCT-US04-02987-198

; Sequence 198, Application PC/TUS0402987

; GENERAL INFORMATION:

; APPLICANT: SENOMYX, INC.

; TITLE OF INVENTION: FUNCTIONAL COUPLING OF T1RS AND T2RS BY GI PROTEINS

; TITLE OF INVENTION: AND CELL-BASED ASSAYS FOR THE IDENTIFICATION OF T1R

; TITLE OF INVENTION: AND T2R MODULATORS

; FILE REFERENCE: 100337.54281WO

; CURRENT APPLICATION NUMBER: PCT/US04/02987

; CURRENT FILING DATE: 2004-02-03

; PRIOR APPLICATION NUMBER: 60/444,172

; PRIOR FILING DATE: 2003-02-03

; PRIOR APPLICATION NUMBER: 60/457,318

; PRIOR FILING DATE: 2003-03-26

; NUMBER OF SEQ ID NOS: 210

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 198

; LENGTH: 839

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US04-02987-198

Query Match 100.0%; Score 4443; DB 1; Length 839;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MGPRAKTICSLFLLWVLAEPANSDFYLPDGYLLGGLFSLHANMKGIVHLNFLQVPMCK 60
      |||
Db      1 MGPRAKTICSLFLLWVLAEPANSDFYLPDGYLLGGLFSLHANMKGIVHLNFLQVPMCK 60

Qy     61 EYEVKVGIGYNLMQAMRFVVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120
      |||
Db     61 EYEVKVGIGYNLMQAMRFVVEEINNDSSLLPGVLLGYEIVDVCYISNNVQPVLYFLAHEDN 120

Qy    121 LLPIQEDYSNYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELKVRFPAL 180
      |||
Db    121 LLPIQEDYSNYISRVVAVIGPDNSESVMTVANFLSLFLLPQITYSAISDELKVRFPAL 180

Qy    181 LRTTPSADHHVEAMVQLMHLFRWNWIIVLVSSDITYGRDNGQLLGERVARRDICI AFQETL 240
      |||
Db    181 LRTTPSADHHVEAMVQLMHLFRWNWIIVLVSSDITYGRDNGQLLGERVARRDICI AFQETL 240

Qy    241 PTLQPNQNMTEERQRLVTIIVDKLQQSTARVVVVFSPDLTLYHFFNEVLRQNFTGAVWIA 300
      |||
Db    241 PTLQPNQNMTEERQRLVTIIVDKLQQSTARVVVVFSPDLTLYHFFNEVLRQNFTGAVWIA 300

Qy    301 SESWAIDPVLHNLTELGHGLTFLGITIQSVPPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360
      |||
Db    301 SESWAIDPVLHNLTELGHGLTFLGITIQSVPPIPGFSEFREWGPQAGPPPLSRTSQSYTCN 360

Qy    361 QECDNCLNATLSFNTILRLSGERVVSVYSAVYAVAHALHSLGCDKSTCTKRVPVYPWQL 420
      |||
Db    361 QECDNCLNATLSFNTILRLSGERVVSVYSAVYAVAHALHSLGCDKSTCTKRVPVYPWQL 420

Qy    421 LEEIWKVNFTLLDHQIFFDPQGDVALHLEIVQWQWDRSQNPFSVASYYPLQRLKNIQD 480
      |||
Db    421 LEEIWKVNFTLLDHQIFFDPQGDVALHLEIVQWQWDRSQNPFSVASYYPLQRLKNIQD 480

Qy    481 ISWHTVNNTIPMSMCKSRQSQGKKKPVGIHVCCFECIDCLPGTFLNHTEDEYECQACP 540
      |||
Db    481 ISWHTVNNTIPMSMCKSRQSQGKKKPVGIHVCCFECIDCLPGTFLNHTEDEYECQACP 540

Qy    541 NEWSYQSETSCFKRQLVFLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600
      |||
Db    541 NEWSYQSETSCFKRQLVFLEWHEAPTIAVALLAALGFLSTLAILVIFWRHFQTPIVRSAG 600

```



```

Qy      601 GPMCFLMLTLLLVAYMVVPVYVGPPKVSTCLCRQALFPLCFTICISCIAVRSFQIVCAFK 660
        |||
Db      601 GPMCFLMLTLLLVAYMVVPVYVGPPKVSTCLCRQALFPLCFTICISCIAVRSFQIVCAFK 660

Qy      661 MASRFPPraysyWvryQgpyVsmAFITVLKMVIVVIGMLATGLSPtTRTDpDDPKITIVSC 720
        |||
Db      661 MASRFPPraysyWvryQgpyVsmAFITVLKMVIVVIGMLATGLSPtTRTDpDDPKITIVSC 720

Qy      721 NPNYRNSLLFNtSLDLLLLSVVGFSFAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780
        |||
Db      721 NPNYRNSLLFNtSLDLLLLSVVGFSFAYMGKELPTNYNEAKFITLSMTFYFTSSVSLCTFM 780

Qy      781 SAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRRD 839
        |||
Db      781 SAYSGVLVTIVDLLVTVLNLLAISLGYFGPKCYMILFYPERNTPAYFNSMIQGYTMRRD 839

```

## RESULT 2

PCT-US04-25459-6

; Sequence 6, Application PC/TUS0425459

; GENERAL INFORMATION:

; APPLICANT: Senomyx, Inc.

; TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS,

; TITLE OF INVENTION: CELL LINES THAT EXPRESS SAID RECEPTORS, AND TASTE COMPOUNDS

; FILE REFERENCE: 19328.0001P1

; CURRENT APPLICATION NUMBER: PCT/US04/25459

; CURRENT FILING DATE: 2004-08-06

; PRIOR APPLICATION NUMBER: 60/494,071

; PRIOR FILING DATE: 2003-08-06

; PRIOR APPLICATION NUMBER: 60/552,064

; PRIOR FILING DATE: 2004-03-09

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 839

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence; note =

; OTHER INFORMATION: synthetic construct

PCT-US04-25459-6

```

Query Match      100.0%; Score 4443; DB 1; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MGPRAKTICSLFLLWVLAEPaENSDFYLPgDYLLGGLFSLHANMKGIVHLNfLQVPMCK 60
        |||
Db      1 MGPRAKTICSLFLLWVLAEPaENSDFYLPgDYLLGGLFSLHANMKGIVHLNfLQVPMCK 60

Qy      61 EYEVKVIgYNLMQAMrFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQpVLYFLAHEDN 120
        |||
Db      61 EYEVKVIgYNLMQAMrFAVEEINNDSSLLPGVLLGYEIVDVCYISNNVQpVLYFLAHEDN 120

Qy      121 LLPIQEDYSNYISRVVAVIGPDNSesVMTVANfLSLFLLPQITYSaISDELrDKVRFPAL 180
        |||
Db      121 LLPIQEDYSNYISRVVAVIGPDNSesVMTVANfLSLFLLPQITYSaISDELrDKVRFPAL 180

Qy      181 LRTPSADHHVEAMVQLMLHFRWNWIIVLVSSDTYGRDNGQLLGERVARRDICIaFQETL 240
        |||
Db      181 LRTPSADHHVEAMVQLMLHFRWNWIIVLVSSDTYGRDNGQLLGERVARRDICIaFQETL 240

Qy      241 PTLQPNQNMTSEERQRLVTIVDKLQqSTARVVVVFPsDLTLyHFFNEVLrQNFTGaVWIA 300
        |||
Db      241 PTLQPNQNMTSEERQRLVTIVDKLQqSTARVVVVFPsDLTLyHFFNEVLrQNFTGaVWIA 300

Qy      301 SESWAIDpVLHNLtELGHLGTfLGITIQSVPIPGFSEfREWGPQAGPPPLSRTSqsSYTCN 360
        |||
Db      301 SESWAIDpVLHNLtELGHLGTfLGITIQSVPIPGFSEfREWGPQAGPPPLSRTSqsSYTCN 360

Qy      361 QECdNCLNATLSFNtILRLSGERVVYSVYSAVYAvaHALHsLLGCDKStCTKRvVYPWQL 420
        |||
Db      361 QECdNCLNATLSFNtILRLSGERVVYSVYSAVYAvaHALHsLLGCDKStCTKRvVYPWQL 420

Qy      421 LEEIWKNfTLLDHQIFFDpQGDVALHLEIVQWQDRSQNPfQSVASyYPLQRQLKNIQD 480
        |||

```

OM protein - protein search, using sw model

Run on: June 20, 2006, 18:01:30 ; Search time 26 Seconds  
(without alignments)  
1101.734 Million cell updates/sec

Title: US-10-035-045-21  
Perfect score: 4443  
Sequence: 1 MGPRAKTICSLFFLLWLAE.....ERNTPAYFNSMIQGYTMRD 839

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 142608 seqs, 34141942 residues

Total number of hits satisfying chosen parameters: 142608

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US06\_NEW\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US07\_NEW\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US08\_NEW\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US09\_NEW\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US10\_NEW\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US11\_NEW\_COMB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1089	24.5	1027	7	US-11-446-813-2	Sequence 2, Appli
2	1079.5	24.3	1078	7	US-11-242-079-7	Sequence 7, Appli
3	1075	24.2	1079	7	US-11-242-079-8	Sequence 8, Appli
4	1075	24.2	1085	7	US-11-242-079-5	Sequence 5, Appli
5	1065.5	24.0	1078	7	US-11-446-813-30	Sequence 30, Appl
6	1064.5	24.0	1088	7	US-11-242-079-6	Sequence 6, Appli
7	1051	23.7	941	7	US-11-446-813-8	Sequence 8, Appli
8	1051	23.7	941	7	US-11-446-813-14	Sequence 14, Appl
9	1044	23.5	941	7	US-11-446-813-10	Sequence 10, Appl
10	1020	23.0	850	7	US-11-446-813-12	Sequence 12, Appl
11	404.5	9.1	388	7	US-11-446-813-6	Sequence 6, Appli
12	248.5	5.6	197	7	US-11-446-813-4	Sequence 4, Appli
13	180	4.1	960	7	US-11-317-847A-108	Sequence 108, App
14	180	4.1	979	7	US-11-317-847A-172	Sequence 172, App
15	180	4.1	1033	7	US-11-317-847A-174	Sequence 174, App
16	130.5	2.9	885	1	PCT-US06-16533-7	Sequence 7, Appli
17	129.5	2.9	938	6	US-10-222-772A-14	Sequence 14, Appl
18	126	2.8	1007	6	US-10-578-392-13	Sequence 13, Appl
19	119.5	2.7	1002	7	US-11-431-708-355	Sequence 355, App
20	119.5	2.7	1004	7	US-11-431-708-358	Sequence 358, App
21	119.5	2.7	1013	7	US-11-431-708-359	Sequence 359, App
22	119.5	2.7	1013	7	US-11-431-708-360	Sequence 360, App
23	113	2.5	471	7	US-11-431-855-11909	Sequence 11909, A
24	113	2.5	471	7	US-11-431-855-20499	Sequence 20499, A
25	104.5	2.4	2478	7	US-11-431-855-17636	Sequence 17636, A
26	103	2.3	1970	6	US-10-418-772-1	Sequence 1, Appli
27	102.5	2.3	488	7	US-11-431-855-28773	Sequence 28773, A
28	100.5	2.3	441	7	US-11-429-594-86	Sequence 86, Appl
29	100.5	2.3	488	7	US-11-431-855-23001	Sequence 23001, A
30	100	2.3	1115	6	US-10-222-772A-16	Sequence 16, Appl
31	99.5	2.2	376	7	US-11-431-855-4192	Sequence 4192, Ap
32	99.5	2.2	1390	7	US-11-431-708-861	Sequence 861, App

33	99.5	2.2	1390	7	US-11-437-729-1183	Sequence 1183, Ap
34	97	2.2	475	6	US-10-392-219A-5	Sequence 5, Appli
35	97	2.2	507	1	PCT-US06-17162-90	Sequence 90, Appl
36	97	2.2	507	7	US-11-417-264-90	Sequence 90, Appl
37	96	2.2	1499	7	US-11-431-855-23601	Sequence 23601, A
38	96	2.2	1515	7	US-11-431-855-11298	Sequence 11298, A
39	95.5	2.1	319	7	US-11-434-137-2602	Sequence 2602, Ap
40	95.5	2.1	319	7	US-11-434-184-2602	Sequence 2602, Ap
41	95.5	2.1	319	7	US-11-434-203-2602	Sequence 2602, Ap
42	95.5	2.1	319	7	US-11-434-127-2602	Sequence 2602, Ap
43	95.5	2.1	319	7	US-11-434-199-2602	Sequence 2602, Ap
44	95.5	2.1	487	7	US-11-431-855-20992	Sequence 20992, A
45	95.5	2.1	1762	7	US-11-431-855-25593	Sequence 25593, A